

P65#26 -> Genes

DNA sequence 1665 b.p. gaatccggccatc ... caagccgaattc linear

P60-1

1	gaatccggccat	ATG	GCG	GCT	AAA	GAC	GTA	AAA	TTC	GGT	AAC	GAC	GCT	CGT	GTG	AAA	ATG	CTG	CCC	GCC	GTA	AAC	77			
1		M	A	A	K	D	V	K	F	G	N	D	A	R	V	K	M	L	R	G	V	N	21			
78	GTA	CTG	GCA	GAT	GCA	CTG	AAA	GTT	ACC	CTC	GCG	CCA	AAA	GCG	CGT	AAC	GTA	GTT	CTG	GAT	AAA	TCT	TTC	GGT	GCA	152
22	V	L	A	D	A	V	K	V	T	L	G	P	K	G	R	N	V	V	L	D	K	S	F	G	A	46
153	CGG	ACC	ATC	ACT	AAA	GAT	GGT	GTT	TCC	GTA	GCA	CGT	GAA	ATC	GAA	CTG	GAA	GAC	AAG	TTC	GAA	AAC	ATG	GGT	GCG	227
47	P	T	I	T	K	D	G	V	S	V	A	R	E	I	E	L	E	D	K	F	E	N	M	G	A	71
228	CAG	ATG	GTG	AAA	GAA	GTT	GCC	TCT	AAA	GCG	AAC	GAC	GCT	GCA	GCG	GGT	ACC	ACC	GCA	ACC	GTA	CTG	GCT	302		
72	Q	M	V	K	E	V	A	S	K	A	N	D	A	A	G	D	G	T	T	T	A	T	V	L	96	
303	CAG	TCC	ATC	ATC	ACT	GAA	GCC	CTG	AAA	GCC	GTT	GCT	GCG	GCC	ATG	AAC	CGG	ATG	GAT	CTG	AAA	CGT	GGT	ATC	GAC	377
97	Q	S	I	I	T	E	G	L	K	A	V	A	A	G	M	N	P	M	D	L	K	R	G	I	D	121
378	AAA	GCT	GTC	GCT	GCT	GCT	GTT	GAA	GAA	CTG	AAA	GCA	CTG	TCC	GTA	CGG	TGC	TCC	GAC	TCT	AAA	GCT	ATT	GCT	CAG	452
122	K	A	V	A	A	A	V	E	E	L	K	A	L	S	V	P	C	S	D	S	K	A	I	A	Q	146
453	GTT	GGT	ACC	ATC	TCC	GCT	AAC	TCC	GAC	GAA	ACC	GTA	GGT	AAA	CTG	ATC	GCT	GAA	GCG	ATG	GAC	AAA	GTC	GGT	AAA	527
147	V	G	T	I	S	A	N	S	D	E	T	V	G	K	L	I	A	E	A	M	D	K	V	G	K	171
528	GAA	GCC	CTG	ATC	ACC	GTT	GAA	GAC	GGT	ACC	CTG	CGG	GAC	CTG	GAC	GTG	GTT	GAA	GGT	ATG	CAG	TTC	GAC	602		
172	E	G	V	I	T	V	E	D	G	T	G	L	Q	D	E	L	D	V	V	E	G	M	Q	F	D	196
603	CGT	GCC	TAC	CTG	TCT	CCT	TAC	TTC	ATC	AAC	AMG	CCG	GAA	ACT	GGC	GCA	GTA	GAA	TTG	GAA	AGC	CGG	TTC	ATC	CTG	677
197	R	G	Y	L	S	P	Y	F	I	N	K	P	E	T	G	A	V	E	L	E	S	P	F	I	L	221
678	CTG	GCT	GAC	AAG	AAA	ATC	TCC	AAC	ATC	CGC	GAA	ATG	CTG	CCG	GTT	CTG	GAA	GCT	GTC	AAA	GCA	GCC	AAA	CCG	752	
222	L	A	D	K	K	I	S	N	I	R	E	M	L	P	V	L	E	A	V	A	K	A	G	K	P	246
753	CTG	CTG	ATC	ATC	GCT	GAA	GAT	GTT	GAA	GCC	GGC	CTG	GCA	ACT	CTG	GTT	GTT	ATC	ACC	ATG	CGC	GGT	ATC	GTA	827	
247	L	I	I	A	E	D	V	E	G	E	A	L	A	T	L	V	V	N	T	M	R	G	I	V	271	
828	AAA	GTC	GCT	GGG	GTT	AAA	GCA	CCT	GGC	TTC	GGC	GAT	CGT	AAA	GCA	ATG	CTG	CGG	GAT	ATC	GCT	ACC	CTG	ACC	902	
272	K	V	A	A	V	K	A	P	G	F	G	D	R	R	K	A	M	L	Q	D	I	A	T	L	T	296
903	GGT	GGT	ACC	GTT	ATC	TCT	GAA	GAG	ATC	GGT	ATG	GAG	CTG	GAA	GAT	CTG	GGA	GGC	CGG	ATG	GAC	AAA	GTC	GGG	AAA	977
297	D	G	T	V	I	S	E	E	I	G	M	E	L	E	K	A	T	L	E	D	L	G	Q	A	K	321
978	CGC	GTT	GTT	ATC	AAC	AAA	GAT	ACC	ACC	ATC	GAT	GCC	GTC	GCG	GAC	GAA	GCT	GCA	ATC	CAG	GGT	CGC	GTC	1052		
322	R	V	V	I	N	K	D	T	T	T	I	I	D	G	V	G	D	E	A	A	I	Q	G	R	V	346
1053	ACT	CAG	ATT	GCT	CGG	CGG	ATC	GAC	AAA	CTG	GAC	TAT	GAC	GCT	GAT	GAA	AAA	CTG	CGG	CGC	GTC	GCG	AAA	CCG	1127	
347	T	Q	I	R	Q	Q	I	E	E	A	T	S	D	Y	D	R	E	K	L	Q	E	R	V	A	K	371
1128	CTG	GCA	GCC	GGG	GTT	GCG	TTC	AAA	GTT	GCT	GGG	ACT	GAA	GTT	GAA	ATG	AAA	GAG	AAA	GCC	GGC	GTT	1202			
372	L	A	G	G	V	A	V	I	K	V	G	A	A	T	S	E	M	K	E	K	A	R	V	396		
1203	AAA	GAT	GCC	CTG	CAC	GCT	ACC	CGT	GCT	GGG	GCA	GAA	GGC	CTG	GTT	GCT	GCT	GCG	GTC	ATG	CGC	GGT	ATC	GTA	1277	
397	S	D	A	L	H	A	T	R	A	A	V	E	G	V	V	A	G	G	G	V	A	L	I	R	421	
1278	GTA	CGG	TCT	AAA	ATT	GGC	GGC	CTG	AAA	GGT	CAG	AAC	GAA	GAC	CAG	ATC	GTC	AAA	GTT	GGC	CTG	CGC	GCA	1352		
422	V	A	S	K	I	A	G	L	K	G	Q	N	E	D	Q	N	V	G	I	K	V	A	L	R	A	446
1253	ATG	GAA	TCC	CGA	CTG	CAC	ATC	GTA	CTG	AAC	TGC	GGC	GAA	GAG	CGG	TCT	GTA	GTG	GCT	AAC	ACC	CTG	GAA	1427		
447	M	E	S	P	L	R	Q	I	V	L	N	C	G	E	E	P	S	V	V	A	N	T	V	K	471	
1428	GGT	GAC	GCT	AAC	TAC	GCT	TAC	AAC	GCA	ACT	GAA	GAA	TAC	GCG	GAC	ATG	ATG	GAT	GGT	ATC	CTG	GAT	CCA	1502		
472	G	D	G	N	Y	G	Y	N	A	A	T	E	E	Y	G	N	M	I	D	M	G	I	L	D	P	496
1503	ACC	AAA	GTA	ACT	CGT	TCT	GCT	GGT	CTG	CAG	TAC	GCG	GCT	TCT	GTT	GTC	ATG	ATG	ACC	ACC	GGT	ATC	GTC	1577		
497	T	K	V	T	R	S	A	L	Q	Y	A	A	S	V	A	G	L	M	I	T	T	E	C	M	V	521
1578	ACT	GAC	CTG	CGG	AAA	GCG	GAT	GCA	GCT	GAC	TTC	GTT	GCT	GCT	GAT	GTC	GGC	GGC	ATG	ATG	TGA	1652				
522	T	D	L	P	K	G	D	A	P	D	L	G	A	A	G	G	M	G	G	M	G	G	H	M	546	
1653	ccaa	ccgg	ccatc																						1665	

Figure 1

P65#44 -> Genes

DNA sequence 1654 b.p. gaattcgggttc ... aaagccgaattc linear

use to subclone for expression

P60-2

1 gaattcgggttc ATG GCA AAA GAA ATT AAA TTT TCA TCA GAT GCC CGT TCA GCT ATG GTC CGT GTC GAT ATC 77
1 M A K S I A S S D A R S A M V R G V D I 21
78 CTT GCA GAT ACT GTT AAA GTC ACT TTG GGA CCA AAA GGT CGC AAT GTC GTT CTT GAA AAG TCA TTC CGT TCA CCC 152
22 L A D T V X V T L G P K G R N V V L E K S F G S P 46
153 TTG ATT ACC AAT GAC GGT GTG ACT ATT GCC AAA GAA ATT GAA TTA GAA GAC CGT TTT GAA AAT ATG CGT GCA AAA 227
47 L I T N D G V T I A K E I E L E D H F E N M G A K 71
228 TTG GTC TCA GAA GTC GCT TCA AAA ACC AAT GAT ATC GCA GGT GAT GCA ACT ACA ACT GCA ACT GTT TTG ACC GCA 302
72 L V S E V A S K T N D I A G D G T T T A T V L T Q 96
303 GCA ATC GTC CGT GAA GGA ATC AAA AAC GTC ACA GCA GGT GCA AAT GCA ATC GGT ATT CGT CGT GGG ATT GAA ACA 377
97 A I V R E G I K N V T A G A N P I G I R R G I E T 121
378 GCA GTT GGC GCA GCA GTT GAA GCT TTG AAA AAC AAC GTC ATC CCT GTT GGC AAT AAA GAA GCT ATC GCT GCA GTT 452
122 A V A A A V E A L K N N V I P V A N K E A I A Q V 146
453 GCA GCC GTC TCT TCT CGT TCT GAA AAA GTT GGT GAG TAC ATC TCT GAA GCA ATG GAA AAA GTT GGC AAA GAC GGT 527
147 A A V S S R S E K V G E Y I S E A M E K V G K D G 171
528 GTC ATC ACC ATC GAA GAG TCA CGT GGT ATG GAA ACA GAG CTT GAA GTC GTC GAA GGA ATG CGT TTT GAC CGT GGT 602
172 V I T I E E S R G M E T E L E V V E G M Q F D R G 196
603 TAC CTT TCA CGG TAC ATG GTG ACA GAT AGC GAA AAA ATG GTG GCT GAC CTT GAA AAT CGG TAC ATT TTG ATT ACA 677
197 Y L S Q Y M V T D S E K M V A D L E N P Y I L I T 221
678 GAC AAG AAA ATT TCC AAT ATC GAA GAA ATC TTG CCA CTT TTG GAA AGC ATT CTC GAA AGC AAT CGT CCA CGC TTG 752
222 D K K I S N I Q E I L P L L E S I L - Q S N R P L L 246
753 ATT ATT GCG GAT GAT GTG GAT GGT GAG GCT CTT GCA ACT CTT GTT TTG AAC AAG ATT CGT GGA ACC TTC AAC GTC 827
247 I I A D D V D G E A L P T L V L N K I R G T F N V 271
828 GTC GCA GTC AAG GCA CCT GGT TTG GAC CGT CGC AAA GGC ATG CTT GAA GAT ATC GGC ATC TTA ACA GGC GGA 902
273 V A V K A P G F G D R R K A M L E D I A I L T G G 296
903 ACA GTT ATC ACA GAA GAC CTT GGT CTT GAG TTG AAA GAT GCG ACA ATT GAA GCT CTT GGT CAA GCA GCG AGA GTG 977
297 T V I T E D L G L E L K D A T I E A L G Q A A R V 321
978 ACC GTG GAC AAA GAT AGC ACG GTT ATT GTC GAA GGT GCA GGA AAT CCT GAA GCG ATT TCT CAC CGT GTT GCG GTT 1052
322 T V D K D S T V I V E G A G N P E A I S H R V A V 346
1053 ATC AAG TCT CAA ATC GAA ACT ACA ACT TCT GAA TTT GAC CGT GAA AAA TTG GCA GAA CGC TTG GCC AAA TTG TCA 1127
347 I K S Q I E T T T S E F D R E K L Q E R L A K L S 371
1128 GGT GGT GTC GCA GGT ATT AAG GTC GGA GCG ACT GAA ACT GAG TTG AAA GAA ATG AAA CTC CGC ATT GAA GAT 1202
372 G G V A V I K V G A A T E T E L K E M K L R I E D 396
1203 GCG CTC AAC GCT ACT CGT GCA GGT GTT GAA GAA GGT ATT GTT GCA GGT GGT GGA ACA GCA GCT CTT GCC AAT GTG ATT 1277
397 A L N A T R A A V E E G I V A G G G T A L A N V I 421
1278 GCA GCT GTT GCT ACC TTG GAA TTG ACA GGA GAT GAA GCA ACA GGA CGT AAT ATT GTT CTC CGT GCT TTG GAA GAA 1352
422 P A V A T L E L T G D E A T G R N I V L R A L E E 446
1353 GGT GTT CGT GCA ATT GCT GCA AAT GCA GGA TTT GAA GGA TCT ATC GTT ATC GAT CGT TTG AAA AAT GCT GAG CTT 1427
447 P V R Q I A H N A G F E G S I V I D R L K N A E L 471
1428 GGT ATA GGA TTC AAG GCA GCA ACT GGC GAG TGG GTT AAC ATG ATT GAT GAA GGT ATC ATT GAT GCA GTT AAA GTG 1502
472 G I G F N A A T G E W V N M I D Q G I I D P V K V 496
1503 AGT CGT TCA GGC CTC CAA AAT GCA GCA TCT GTC GCA AGC TTG ATT TTG ACA ACA GAA GCA GTC GTC GCA GCG AAT AAA 1577
497 S R S A L Q N A A S V A S L I L T T E A V V A N K 521
1578 GCA GAA CCA GTC GCA GGC CCA GGT CCA GCA ATG GAT GCA AGT ATG ATG CGT CGA ATG GCG GGC GGA TGA ~~ccaaagccgaattc~~ 1654
522 P E P V A P A M D P S M H G G M G G 542

Figure 2

Y65#5 -> Genes

DNA sequence 1662 b.p. gaattcgggtttatc ... caagccgaaatc linear

Y60-1

1 gaattcgggtttatc ATG CGG CCT AAA GAT GTC AAA TTC GGT AAC GAC CCT CGT GTC AAA ATG CTC CGC GGC GTC AAC 77
M A A K D V K F G N D A R V K M L R G V N 21
78 GTC CTG GCA GAC GCA GTT AAA GTC ACC CTG GGC CGG AAA GGC CGT AAC GTC CTG CTG GAC AAA TCC TTC GGC GCG 152
22 V L A D A Y K V T L G P K G R N V V L D K S F G A 46
153 CCA ACC ATC ACC AAA GAT GGT GTT TCT GTC GCA CGT GAA ATC GAG CTG GAA GAC AAG TTC GAA AAC ATG GGC GCG 227
47 P T I T K D G V S V A R E I E L E D K F E N M G A 71
228 CGG ATG GTG AAA GAA GTG GCG TCT AAA GCG AAC GAC CCT GCA CGC GAC GGT ACC ACC ACC GCG ACC GTG CTG CCT 302
72 Q M V K E V A S K A N D A A G D G T T T A T V L A 96
303 CGG GCT ATC ATC ACC GAA GGT CTG AAA GCG GTT CCT GCG GGC ATG AAC CCA ATG GAT CTG AAA CGT GGT ATC GAC 377
97 Q A I I T E G L K A V A A G M N P M D L K R G I D 121
378 AAA GCT GTC CGG TCC CCT GTT GAA GAA CTG AAA GCG CTG TCC GTC CGG TCC TCT GAC TCT AAA GCG ATT GCT CGG 452
122 K A V A S A V E E L K A L S V P C S D S K A I A Q 146
453 GTC GGT ACC ATC TCC CCT GTT AAC GTC GAA ACC GTC GGT AAA CTG ATC GCG GAA CGG ATG GAT AAA GTC GGT AAA 527
147 V G T I S A N S D E T V G K L I A E A M D K V G K 171
528 GAA GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT CTG GAA GAC GAA CTG GAC GTG GTT GAA GGT ATG CGG TTC GAC 602
172 E G V I T V E D G T G L E D E L D V V E G M Q F D 196
603 CGG GGT TAC CTG TCC CCA TAC TTC ATC AAC AAG CCA GAA ACT GGC GCT GTT GAG CTG GAA AGC CGG TTC ATC CTG 677
197 R G Y L S P Y F I N K P E T G A V E L E S P F I L 221
678 CTG GCT GAC AAG AAA ATC TCC AAC ATC CGC GAA ATG CTG CCA GTG CTG GAA GCG GTT GCG AAA CGA CGC AAA CGG 752
222 L A D K K I S N I R E M L P V L E A V A K A G K P 246
753 CTG GTT ATC ATT GCT GAA GAC GTT GAA GGC GAA CGG CTG CGG ACC CTG GTG GTT AAC ACC ATG CGT GGC ATC CTG 827
247 L V I I A E D V E G E A L A T L V V N T M R G I V 271
828 AAA GTG GCT CGG GTT AAA GCA CCT GGC TTC GGC GAC CGC CGT AAA GCG ATG CTG CAG GAT ATC GCT ACC CTG ACC 902
372 K V A A V K A P G F D R R K A M L Q D I A T L T 296
903 GGC GGT ACC GTC ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCG ACC CTG GAA GAC CTG CGC CGG GCT AAA 977
397 G G T V I S E E I G M E L E K A T L E D L G Q A K 321
978 CGT GTT GTG ATC AAC AAA GAC ACC ACC ATC GAT GGC GTG GGC GAC GAA GCG GCG ATT CGG CGT GTT 1052
322 R V V I N K D T T T I I D G V G D E A A I Q G R V 346
1053 GGT CGT ATC CGT AAG CGG ATC GAA GAA CGC ACT TCC GAT TAC GAC CGT GAA AAA CTG CAG GAG CGG GTC GCA CGG AAA 1127
347 G Q I R K Q I E E A T S D Y D R E K L Q E R V A K 371
1128 CTG CGA CGC CGT GTT CGG GTC ATC AAA GTC CGT GCT CGG ACT GAA GTT GAA ATG AAA GAG AAA AAA CGA CGC GTT 1202
372 L A G G V A V I K V G A A T E V E M K E K K A R V 396
1203 GAC GAT CGC CTG CGC CGG ACC CGT GCT CGG GTC GAA GAA CGC GTG GTT GCT GGT GGT GTG CGG CTG CTG CGT 1277
373 D D A L H A T R A A V E E G V V A G G G V A L V R 421
1278 GTT CGC CGG AAA CTG TCC CGC CTG ACT GGT CGG AAC GAC GAA GAT CGG AAC GTG GGT ATC AAA GTT CGG CTG CGC CGA 1352
422 V A A K L S G E T A Q N E D Q N V G I K V A L R A 446
1353 ATG GAA GCT CGA CTG CGT CGC ATC CGG TCC AAC GCG GGT GAA GAG CGA CCT TCT GTT GTG ACC AAC AAC GTG AAA CGA 1427
447 M E A P L R Q I V S N A G E E P S V V T N N V K A 471
1428 CGC GAA GGT AAC TTA CGT TAC AAC CGA CGA ACT GAA GAA TAC CGC AAC ATG ATC GAC TTC GGT ATC CTG GAT CGA 1502
472 G E G N Y G Y N A A T E E Y G N M I D F G I L D P 496
1503 ACC AAA GTG ACC CGT TCT GCT CTG CGG TAC CGC CGA TCT GTC GCT CGC CTG ATG ATC ACC ACC GAG CGC CGT ATG GTG 1577
497 T K V T R S A L Q Y A A S V A G L M I T T E C M V 521
1578 ACC GAC CTG CCT AAA CGC GAC CGA CCT GAC TTA CGT GCT CGA CGC ATG CGG CGT CGG CGT ATG ATG TGA CGAA 1653
522 T D L P K G D A P D L G A A G M G G M G G M M 545
1654 gcccggatc 1662

Figure 3

Y65#21 -> Genes

DNA sequence 1661 b.p. gaattcgggttc ... TAAGccgaattc linear

V261 - same in clone Y65#24, too
used to subclone for expression !!!

Y60-2

1 gaattcgggttc ATG GCA AAA GAA ATC AAA TTT TCA GCA GAT GCG CGT GCT GCC ATG GTG CCC GGA GTT GAT ATG 77
1 M A K E A K F S A D A R A A M V R G V D M 21
78 TTA GCA GAT ACC GTC AAA GTC ACC CTT GGT CCT AAA CGG CGC AAT GTC GTC CTT GAA AAA GCT TTT GGT TCT CCC 152
22 L A D T V K V T L G P K G R N V V L E K A F G S P 46
153 TTA ATT ACT AAT GAC CGG GTC ACC ATT GCT AAA GAG ATC GAA TTA GAA GAT CAT TTT GAA AAC ATG GGA GCA AAA 227
47 L I T N D G V T I A K E I E L E D H F E N M G A K 71
228 TTG GTG TCT GAA GTG CCT TCT AAA ACC AAT GAT ATT GCT GGT GAT CGG ACC ACT ACT GCA ACA GTT TTG ACA CAA 302
72 L V S E V A S K T N D I A G D G T T T A T V L T Q 96
303 GCC ATT GTT CAT GAA CGA CTC AAA ATT GTG ACA GCA GGT GCT AAT CCA ATT GGT ATC CGT CGA GGC ATT GAA ACA 377
97 A I V H E G L K N V T A G A N P I G I R R G I E T 121
378 GCA ACA GCA ACA GCT GTT GAA CGC TTG AAA GGC ATT GCT CCA CCT GTC TCT GGC AAG GAA GCT ATT GCT CAG GTC 452
122 A T A T A V E A L K A I A Q P V S G R E A I A Q V 146
453 GCT GCA GTC TCA CGC TCT GAA AAA GTT GGA GAG TAT ATC TCA GAA GCT ATT GAG CGT TTG GGC AAC GAT GGT 527
147 A A V S S R S E K V G E Y I S E A M E R V G N D G 171
528 GTG ATT ACC ATC GAA GAA TCT CGA GGT ATG GAA ACA GAA CCT GTG GTT GAA GGC ATT GCA ATT GAC CGT GGT 602
172 V I T I E E S R G M E T E L E V V E G M Q F D R G 196
603 TAC CTG TCT CAA TAC ATG GTC ACA GAC ATT GAA AAA ATT GTT GCA GAC CTT GAA ATT ATC TCA ATT ATC ACC 677
197 Y L S Q Y M V T D N E K M V A D L E N P F I L I T 221
678 GAT AAA AAA GTG TCA AAC ATC GAA GAC ATT TTG CCA CTC CTT GAG GAA GTT CTT AAA ACC AAC CGT CCA TTA CTC 752
222 D K K V S N I Q D I L P L L E E V L K T N R P L L 246
753 ATT ATT GCA GAT GAT GTG GAT GGT GAA GCA CTT CCA ACC CTT GTC TTG AAC AAG ATT CGT GGT ACT TTC ATT GTG 827
247 I I A D D V D G E A L P T L V L N K I R G T F N V 271
828 GTT GCT GTC AAA CGG CCA GGA TTT GGT GAT CGT CGT AAA GCT ATT GTC CTT GAA GAC ATT GCT ATT TTG ACA GGT GGT 902
272 V A V K A P G F G D R R K A M L E D I A I L T G G 296
903 ACA GTG ATT ACA GAG GAT CTC GGA CTT GAA TTA AAA GAT GCT ACA ATT ACA GGC CTT GGA CAG GCT GCT AAG ATT 977
297 T V I T E D L G L E L K D A T M T A L G Q A A K I 321
978 ACA GTT GAT AAA GAT ACC ACA GTC ATT GTT GAA GGT TCA GGA AGT TCA GAA GCT ATT GCT AAC CGT ATT GCA CTG 1052
322 T V D K D S T V I V E G S G S S E A I A N R I A L 346
1052 ATT AAA TCG CAA TTA GAA ACA ACA ACT CCT GAC TTT GAC CGT GAA AAA CTC CAA GAA CGT TTG GCG AAA TTA GCT 1127
347 I K S Q L E T T T S D F D R E K L Q E R L A K L A 371
1128 GGT GGT GTC CCT GTT ATC AAA GTC GGA GCT CCA ACA GAG ACA GCT TTA AAA GAA ATT AAA CCT CGC ATT GAG GAT 1202
373 G G V A V I K V G A P T E T A L K E M K L R I E D 396
1209 GCT CTC ATT GCT ACA CGT GCA GCG CCT GAA GAA GGT ATC CCT GCT GCT GGT GGT GCA ACA GCA CCT ATT ACG GTT ATT 1277
392 A L N A T R A A V E E G I V A G G G T A L I T V I 421
1279 GAA AAA GTC GCA GCT CCT GAG CTT GAG CGC GAT GAT GCT ACT GGA CGT AAC ATT GTG CCT CGT GCT CTC GAA GAG 1352
422 E K V A A L E L E G D D A T G R N I V L R A L E E 446
1353 CCT GTC GCA ATT GCT TTA ATT GCT CGG TAC GAA GCG TCC GTC GTC ATT GAC AAG TTG AAA AAC AAC AGC CCT GCA 1427
447 P V R Q I A L N A G Y E G S V V I D K L R N S P A 471
1428 GGA ACA GGA ATT AAT GCT GCA ACA GGT GAG TGG GTT GAT ATG ATT AAA ACA GGA ATC ATT GAC CGT GTC AAA GTC 1502
472 G T G F N A A T G E W V D M I K T G I I D P V K V 496
1503 ACA CGA TCA CGG CCT CTC AAA ATT GCA GCT CCT GTC GTC GCT AGT CCT ATT TTG ACA ACA GAA GCA CCT TTG GTC ATT AAA 1577
497 T R S A L Q N A A S V A S L I L T T E A V V A N K 521
1578 CCT GAA CGA CGT ACC CGA CGG CGA CGA ATG CGA CGA GGT ATG GAT CGA CGA ATG ATG GGT GGG ATG GGC CGA TAA 1652
522 P E P A T P A P A M P A G M D P G M M G G M G G Δ 546
1653 gcccgaattc

1661

Figure 4

Sequencing strategy (scale : 1cm = approx. 100bp)

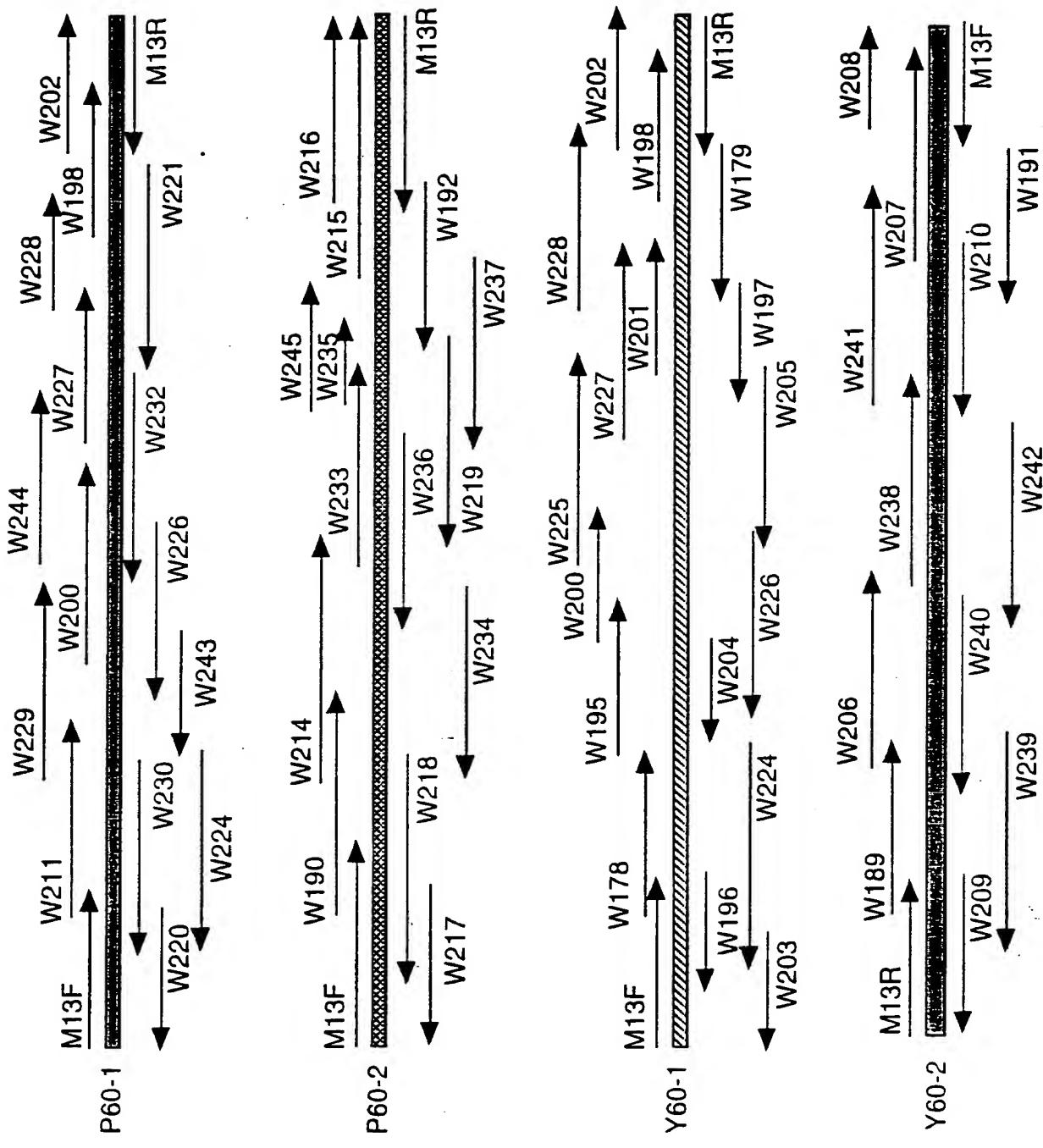


Figure 5

T7 expression construct of His-tagged *Streptococcus pneumoniae* hsp60-1
PCR product starts at NdeI (58) site and ends at EcoRI site (1706)

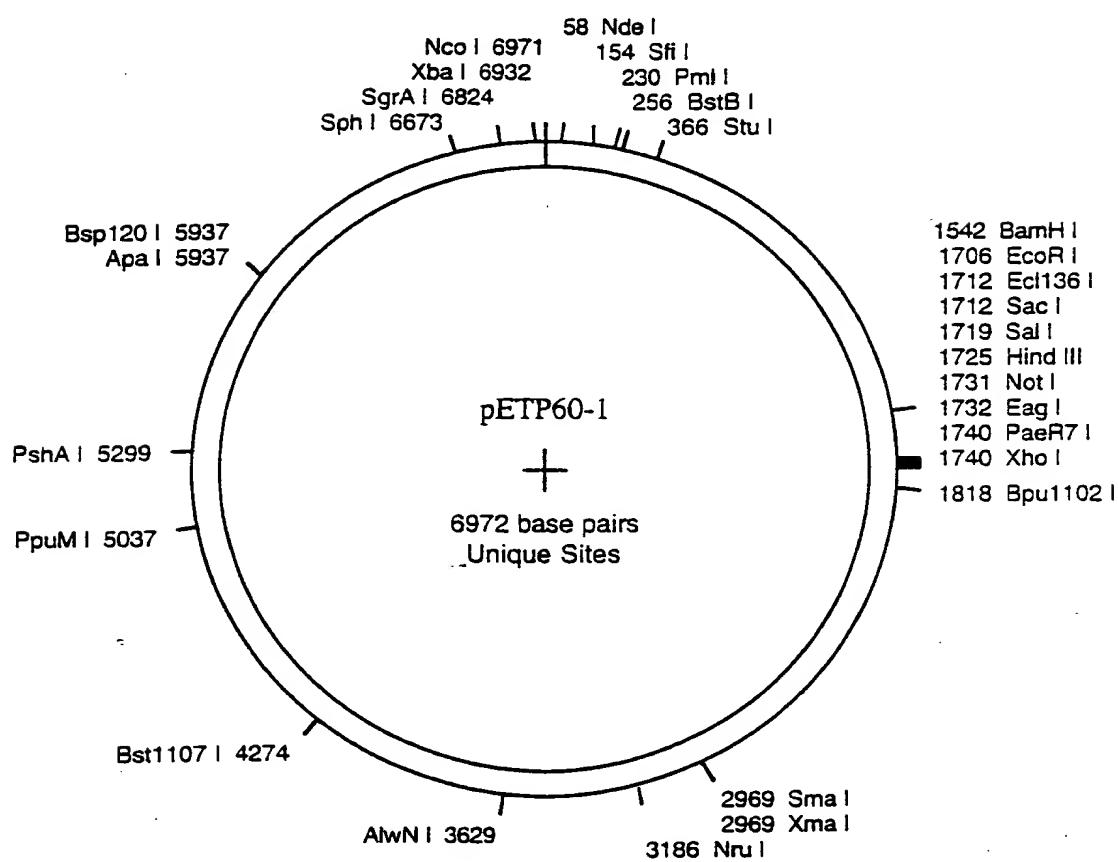


Figure 6

T7 expression construct of His-tagged *Streptococcus pneumoniae* hsp60-2
PCR product starts at NdeI (58) site and ends at EcoRI site (1695)

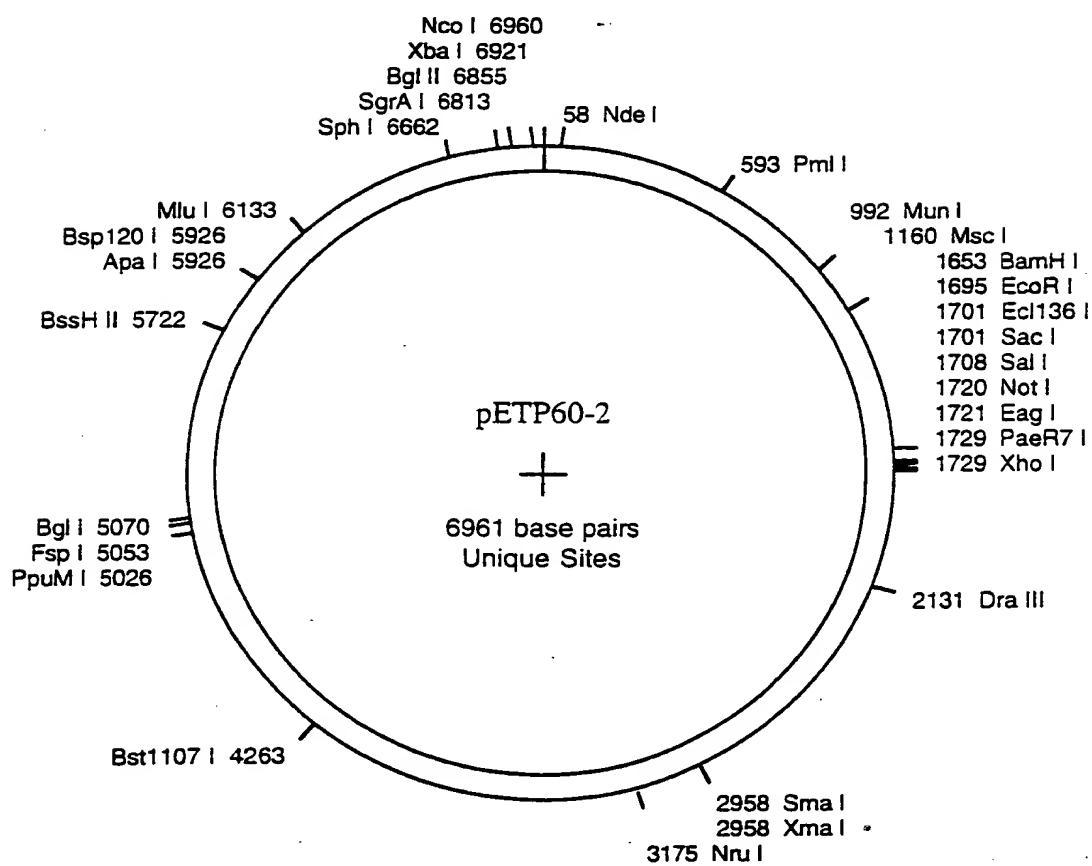


Figure 7

T7 expression construct of His-tagged *Streptococcus pyogenes* hsp60-1
PCR product starts at NdeI (58) site and ends at EcoRI site (1703)

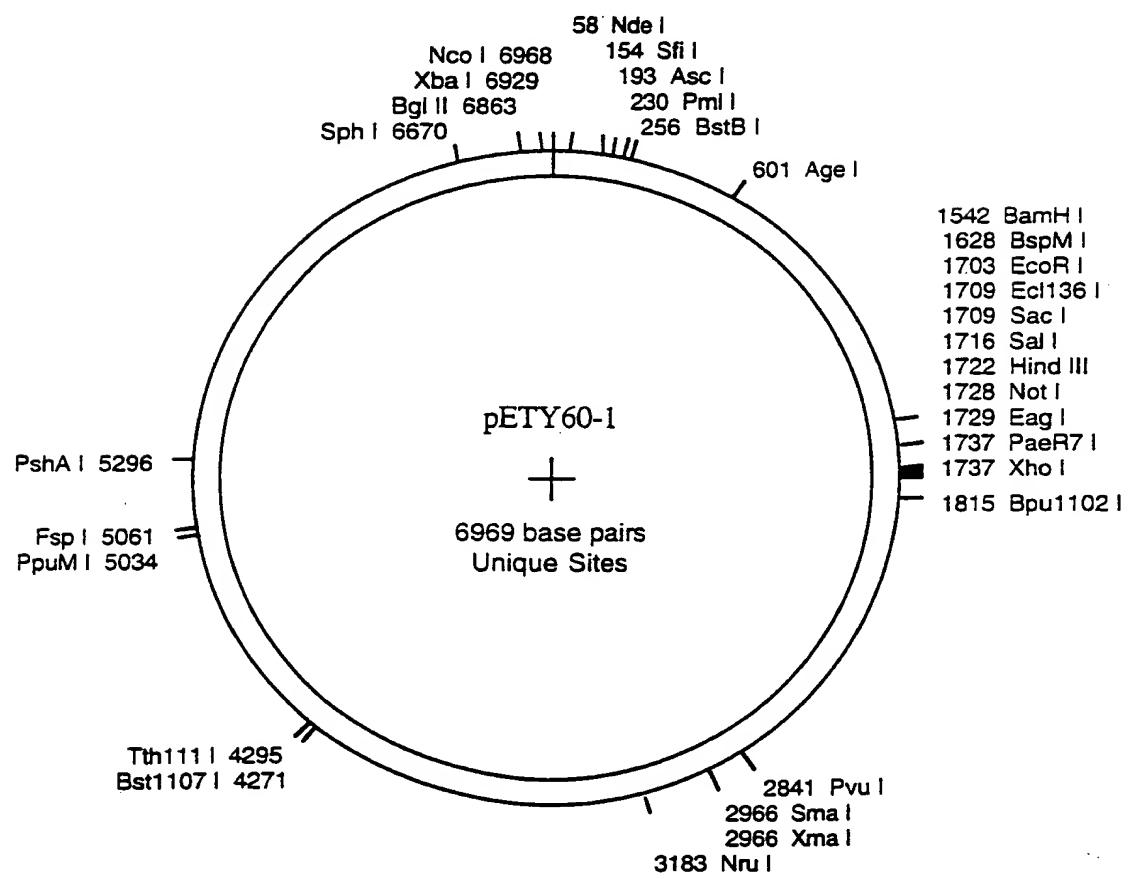


Figure 8

T7 expression construct of His-tagged *Streptococcus pyogenes* hsp60-2
PCR product starts at NdeI (58) site and ends at EcoRI site (1702)

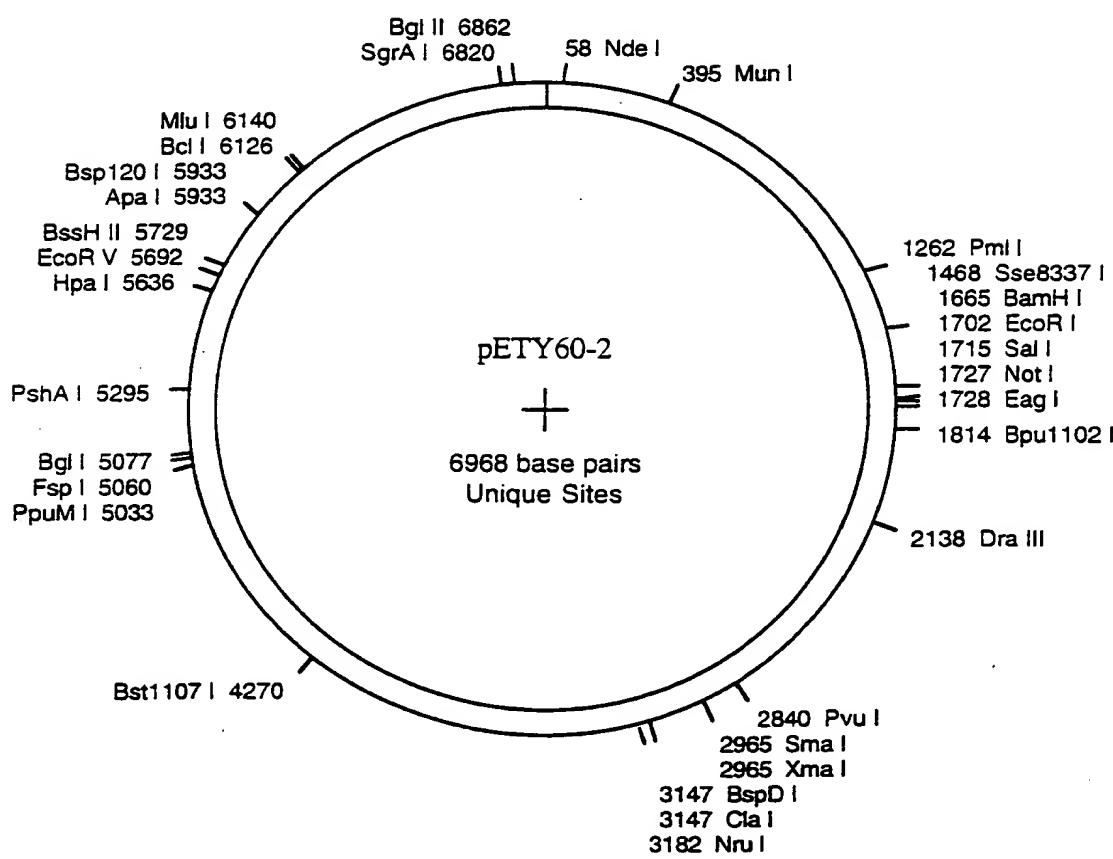


Figure 9

MA	MA	-KDIKFGEEARRMLRGVNALLADAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>S. pneumoniae</i> hs MA	10	-AKDVKFGENDAVKVTLGPNVNLLADAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>S. pyogenes</i> hs MA	20	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>S. pneumoniae</i> MA	30	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>S. pyogenes</i> hs MA	40	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>B. subtilis</i> gr MA	50	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>Clostridium</i> h MA	60	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>Cowdria</i> hsp60 MA	70	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>Haemophilus</i> h MA	80	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>L. pneumophila</i> MA	90	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>M. avium</i> hsp60 MA	100	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>M. bovis</i> hsp60 MA	110	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>M. leprae</i> groE MA	120	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>M. leprae</i> hsp6 MA	130	-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>M. tuberculosis</i> MS		-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>N. meningitidis</i> MA		-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>S. aureus</i> hsp6 MA		-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>Synechocystis</i> MA		-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>Tsukamurella</i> MA		-AKDVKFGENDAVKVTLGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>S. pombe</i> hsp60 M		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>S. cerevisiae</i> M		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>P. falciparum</i> M		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>Onchocerca</i> hs MTNV		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>C. elegans</i> hsp M		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>D. melanogaster</i> M		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
human hsp60		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
<i>Arabidopsis</i> h M		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
malzze hsp60		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV
RUBISCO		-VSFLSS--SVSRLPLRAGRIPGREAPVQVIT--Y--A--KDLRKEGDARASLITGPKGRNVWLEKSFGAPTLTKDGVITVAKERIELEDDKFENGAGQLVKEVASKTNDV

Figure 10A

Figure 10B

Figure 10C

TSEKQKAELEDPLIITDKISNQDILIPPLEEVA--QAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSLEDATLED-LQAKKVVTKDDTT						
270	290	300	310	320	330	340
S. pneumoniae	NRPETGAVELESPILLDKISNIREMLVLEAVA--KAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSLEDATLED-LQAKKVVTKDDTT	331				
S. pyogenes	NRPETGAVELESPILLDKISNIREMLVLEAVA--KAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSLEDATLED-LQAKKVVTKDDTT	331				
S. pneumoniae	TDSEKQKADLENPILITDKISNQDILIPPLESTI--QSNRPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSLEDATLED-LQAKKVVTKDDTT	329				
S. pyogenes	TDNEKQADLENPILITDKISNQDILIPPLESTI--KTNRPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSLEDATLED-LQAKKVVTKDDTT	329				
B. subtilis	hsp60 TDSRKNEAVLDNPYILITDKISNQDILIPPLEQV--QZGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSLEDATLED-LQAKKVVTKDDTT	329				
Clostridium h	TDTERKEAVLDNPYILITDKISNQDILIPPLEQV--QAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSLEDATLED-LQAKKVVTKDDTT	329				
Haemophilus h	NPKETATVLDNPYILITDKISNQDILIPPLEQV--RSGRELIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSLEDATLED-LQAKKVVTKDDTT	332				
Leptospirilla	hsp60 TNSERKMLVEFNPYILITDKISNQDILIPPLEQV--KAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSLEDATLED-LQAKKVVTKDDTT	331				
M. avium	hsp60 TDAERQEALEDPPFLUVSSRKSTVDKLIPPLEKVI--QAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-VGSLSESADISL-LGKARKVVTKDDTT	330				
M. bovis	hsp60 TDPERQEALEDPPFLUVSSRKSTVDKLIPPLEKVI--GAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-VGSLSESADISL-LGKARKVVTKDDTT	329				
M. leprae	groE TDFDSQAVLDPLVLIQOEKISSLPPLMPEKVI--ESGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-VGSLSESADISL-LGKARKVVTKDDTT	329				
M. leprae	hsp6 TDAERQEALEDPPFLUVSSRKSTVDKLIPPLEKVI--QAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-VGSLSESADISL-LGKARKVVTKDDTT	329				
M. tuberculosis	TDFDNQCAVLDPLVLIQDKISSLPPLMPEKVI--GAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-VGSLSESADISL-LGKARKVVTKDDTT	329				
N. meningitidis	NDAEKQAGLNDPPEVLDPLVLIQDKISSLPPLMPEKVI--KASRPPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-VGSLSESADISL-LGKARKVVTKDDTT	329				
S. aureus	hsp6 TDSDKMVAELERPLVLDKISSFDQILIPPLEQV--QSNRPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-VGSLSESADISL-LGKARKVVTKDDTT	331				
Synechocystis	TDSEKQKADLENPILITDKISNQDILIPPLEQV--QZGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	330				
Synechocystis	TDSDRQVEFDPNPLIITDKISNQDILIPPLEQV--RZGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	330				
Tsukamurella	TAERQEALEDPPFLUVSSRKSTVDKLIPPLEKVI--QSGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	329				
S. pombe	hsp60 TWSKQKVEFPLIITDKISNQDILIPPLEQV--ELANQ--RPLVIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	329				
S. cerevisiae	TDPKSSKVEFPLIITDKISNQDILIPPLEQV--ELSNQ--RPLVIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	362				
P. falciparum	NN--SOKVELDKPVLIIHEKISTVSKSLIPPLEH--LONQSSILVIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	352				
Onchocerca	hsp60 TNSKQKCEPDLIITDKISNQDILIPPLEQV--ELANAH--RPLVIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	356				
C. elegans	hsp60 TSGAKVEYKAVLISERKISQDVIPAL--ELANKL--RPLVIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	347				
D. melanogaster	NSSKGNKVEFODMLLSEKVISSKQDILIPPLEQV--ELANAH--RPLVIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	347				
human	hsp60 NTSGQKCEFDQYDVLLEKISSKQDILIPPLEQV--ELANAH--RPLVIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	357				
Arabidopsis	h TNGQTKCEPDLIITDKISNQDILIPPLEQV--ELALKR--ORPLLIVSEVEDSEALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	356				
maize	hsp60 TNSKAQKCEPDLIITDKISNQDILIPPLEQV--ELALKR--ORPLLIVSEVEDSEALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	361				
RUBISCO	ChaperoneNSPEKSIIVEARVLTQDPLKISAIKDLIPPLEKVI--QZAGKPLIIIAEDV3EALATLVNKLRGLTVVAKVAPGFDGRKMLQDIAILITGGQVISEE-LGSARRNTKDDTT	364				

Figure 10D

IVDGAGD--AAIAGRAVQIQRSEEST-SPYDKEKUQERLAKVKGAAATEVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NGDEATGVNIVLRAEPLRQIAE						
400	410	420	430	440	450	460
470	480	490	500	510	520	
<i>S. pneumoniae</i> IVDGAGD--AAIAGRAVQIQRSEEST-SPYDKEKUQERLAKVKGAAATEVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NGDEATGVNIVLRAEPLRQIAE						
<i>S. pneumoniae</i> hs IVDGAGD--AAIAGRAVQIQRSEEST-SPYDKEKUQERLAKVKGAAATEVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NGDEATGVNIVLRAEPLRQIAE						
<i>S. pneumoniae</i> IVEGAGN--DEAISURVAVIKSQQLEETT-SEFDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDEATGVNIVLRAEPLRQIAE						
<i>S. pneumoniae</i> hs IVEGAGS--SEAIAANRALIQLIKSQQLEETT-SEFDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDDATCRNIVLRAEPLRQIAE						
B. subtilis gr IVEGAGE--TUKISARUTQIRAOLEETT-SEFDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDNQTCGIVNIVLRAEPLRQIAE						
Clostridium h IVEGAGN--SEEIKNRINQIQLKQLEETT-SEFDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--IODEQVGIVNIVLRAEPLRQIAE						
Cowdria hsp60 II-GSVNCSAVQSRICOINHOLDNST-SEYDKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NDEQOLGIVNIVLRAEPLRQIAE						
Haemophilus h IVDGIGD--EIQIGRVAQIQRQIEEST-SEYDKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEFFONVGKUQKALRAMEAPLQIWA						
<i>L. pneumophila</i> IVDGRK--ATEINARITQIRQMEETT-SEYDREKUQERVAKLQAGGAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NDDQMGINNLRRAIESPQRQIVT						
<i>M. avium</i> hsp60 IVEGAGD--SDAIAGRVAQIRTEIENS-SEYDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GEEATGANTIVVRALEPLQIWF						
<i>M. bovis</i> hsp60 IVEGAGD--SDAIAGRVAQIRTEIENS-SEYDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GHEATGANTIVVRALEPLQIWF						
<i>M. leprae</i> groE IVDGGG--SNDAVAKRNQNLRAEIEVSD-SEYDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDEALGIDVFEFEALKAPLYWIAF						
<i>M. leprae</i> hsp6 IVEGAGD--SDAIAGRVAQIRTEIENS-SEYDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDEATGANTIVVRALEPLQIWF						
<i>M. tuberculosis</i> IVDGGG--TAEAVANRAKHLRAEIDKS--SDWDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDEATGANTIVVRALEPLQIWF						
<i>N. meningitidis</i> IVDGFGD--ANQIEMARVNEITQIETAT-SEYDKEKUQERVAKLQAGGAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NADODAGVOTVLRATVSPQRQIWA						
<i>S. aureus</i> hsp6 IVDGDD--ENSIDARVSOLSOIETE-SEFDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDEATGANTIVVRALEPLQIWF						
<i>S. aureus</i> hsp6 IVDGDD--ENSIDARVSOLSOIETE-SEFDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDEATGANTIVVRALEPLQIWF						
<i>S. enterocystis</i> IVAEGNE--AVVKSRCRQKPSASVURKQYEAASD-SEYDKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDEATGANTIVVRALEPLQIWF						
<i>S. enterocystis</i> IVAEGNE--AVVKSRCRQKPSASVURKQYEAASD-SEYDKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDEATGANTIVVRALEPLQIWF						
<i>Trsukamurella</i> IVDGAGS--KEQIAGRVSQIARTEIENS-SEYDREKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--GDEATGANTIVVRALEPLQIWF						
<i>S. pombe</i> hsp60 IMKGAGD--VKNDRCEQIIGVIMADPNLUTSESEKELQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
<i>S. cerevisiae</i> IINGSPK--EAQERIEIQRSIDITINNSYEKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
<i>P. falciparum</i> IMEGEGPK--EINERCESTINAIRMT--SYEKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
<i>Onchocerca</i> hs IV--SE-NRVTDRVKRQKARIEQINSQIESST-SDYDKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
<i>C. elegans</i> hsp IJRGGRGQ--TEIKRRIEETDEIERST-SYEKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
<i>D. melanogaster</i> LLKGKPK--DVILRANQITKIEDTT--SEYEKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
human hsp60 LLKGKGDK--AQIQTKEIIEQDVT--SEYEKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
Arabidopsis h IVDGAGD--KGIERCEQIFSAIELST-SDYDKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
maize hsp60 IVDGADK--KSIIEERAOIISAVNST-SDYDKEKUQERLAKVKGAAVAVIKLACQGAVAVIKLACQKEDALNATRAAVEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
RUBISCO chaper IADASK--DEOSRVAQLKKELSETD-SYDSEKLAERTAKLSGGIVVIVKGAAATELEDRKURIEDAKNNTFMAIEGIVPGGCVALLRAAPALDKLKT--NEDQKLGIVNIVKVKLTKPQIATV						
						503

NAGL005SV-VWERKVN-	SPAG-GYNAATGEYVDMIAAGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-M-	530
<i>S. pneumoniae</i>	NCGRFETSV-VANTVKA---CGDGNYYNAATEEYGNMIDMGILIDFTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	543
<i>S. pyogenes</i> hs	NAGEEEPSV-VINNVKA---CGDGNYYNAATEEYGNMIDFGILIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	544
<i>S. pneumoniae</i>	NAGFPESTI-VIDRUKN---AELGIGFNAATGEYVDMIGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	545
<i>S. pyogenes</i> hs	NAGYEGGSV-VIDRUKN---SPAGTGFNAATGEYVDMIGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	546
<i>B. subtilis</i> gr	NAGL005SV-IVERUKN---BEIGVGFNAATGEYVDMIGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	547
<i>Clostridium</i> h	NAGL005SV-1IEKVN---SDAGVGFDAALRGYEYDMLKAGIYDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	548
<i>Haemophilus</i> h	NAGSERAPCVIAHLLKONDRELI---FNDVDTNFANAFISGVIDPLKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	549
<i>Haemophilus</i> h	NAGEEANSV-1ISAVKVN---GEGNFGYNAATGEYQDMVIGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	550
<i>L. pneumophila</i>	NAGYENSV-VINVKVN---HDNYGFGNAATGEYQDMVIGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	551
<i>M. avium</i>	hsp60 NAGL005SV-VIEKVRN---SPAGTGFNAATGEYDMLKAGIADPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	552
<i>M. bovis</i>	hsp60 NAGL005SV-VIEKVRN---LPAGHGLNAATGEYDMLKAGIADPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	553
<i>M. leprae</i> groE	NAGL005AV-VVDKVSG---LPAGHGLNAATGEYDMLKAGIADPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	554
<i>M. leprae</i> hsp6	NSGR6PSV-VIEKVRN---LSVGHGLNAATGEYDMLKAGIADPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	555
<i>M. tuberculosis</i>	NAGL005SV-VIEKVRN---LPAGHGLNAATGEYDMLKAGIADPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	556
<i>N. meningitidis</i>	NAGEEPSV-VIEKVRN---GKGNIGNAGSSEYDMLKAGIADPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	557
<i>S. aureus</i>	hsp6 NAGL005SV-IVERUKN---AEPGVGFGNATGNTENVNMLRGIVDFTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	558
<i>Synectocystis</i>	NAGCNGAV-1SERVK---KEFNGYNAASLSEYDMLKAGIADPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	559
<i>Synechocystis</i>	NAGYEGGSV-1VEKVK---ATGNQGIVNVTGKLIBDIAAGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	560
<i>Tsukamurella</i>	NAGL005SV-VIEKVRN---SPAGTGFNAATGEYDMLKAGIADPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	561
<i>S. pombe</i>	hsp60 NAGL005SV-IVGKLLKELYKEFNGYDIAKDRFDIINEGVGIDPLKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	562
<i>S. cerevisiae</i>	NAGEEGSV-1IGKL1DEYGDFAKGDFTKVKTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	563
<i>P. falciparum</i>	NAGHEGSV-1VGNILKOKNSNI---GFNAQEGKVTDMSGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	564
<i>Onchocerca</i> hs	NAGLESAV-1IDYL1KQNNKELI---YNEVAMSYANAFAGVIDPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	565
<i>C. elegans</i> hsp	NAGLEPSS-1IDEVTKGNTSY---GYDALANGKFDVDFEAGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	566
<i>D. melanogaster</i>	NAGTGDAN-VVAKVENQG-DY---GYDA-KGEVGNLIEKGIDFTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	567
human	hsp60 NNGVEGSL-1VEKIM-QSSSEV---GYDAMAGDFVNVEGLIDPTKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	568
<i>Arabidopsis</i> h	NAGVEGAV-1VGGKLLEQTNPDL---GYDAAKGEYDVMVKGAGLIDPLKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	569
maize	hsp60 NNGVEGAV-1VGGKLLEQTNPDL---GYDAAKGEYDVMVKGAGLIDPLKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	570
RUBISCO chaper	NAGIEGEV-VIEKVRN---GEVGYNAMMTYENLVESEVIDPKVTRSLQNAASVASLMLTTEAVVVDKPEKEAAPAG-MPGCM--M-GEMCGNGGM-	571

Figure 10E

Current Chromatogram(s)

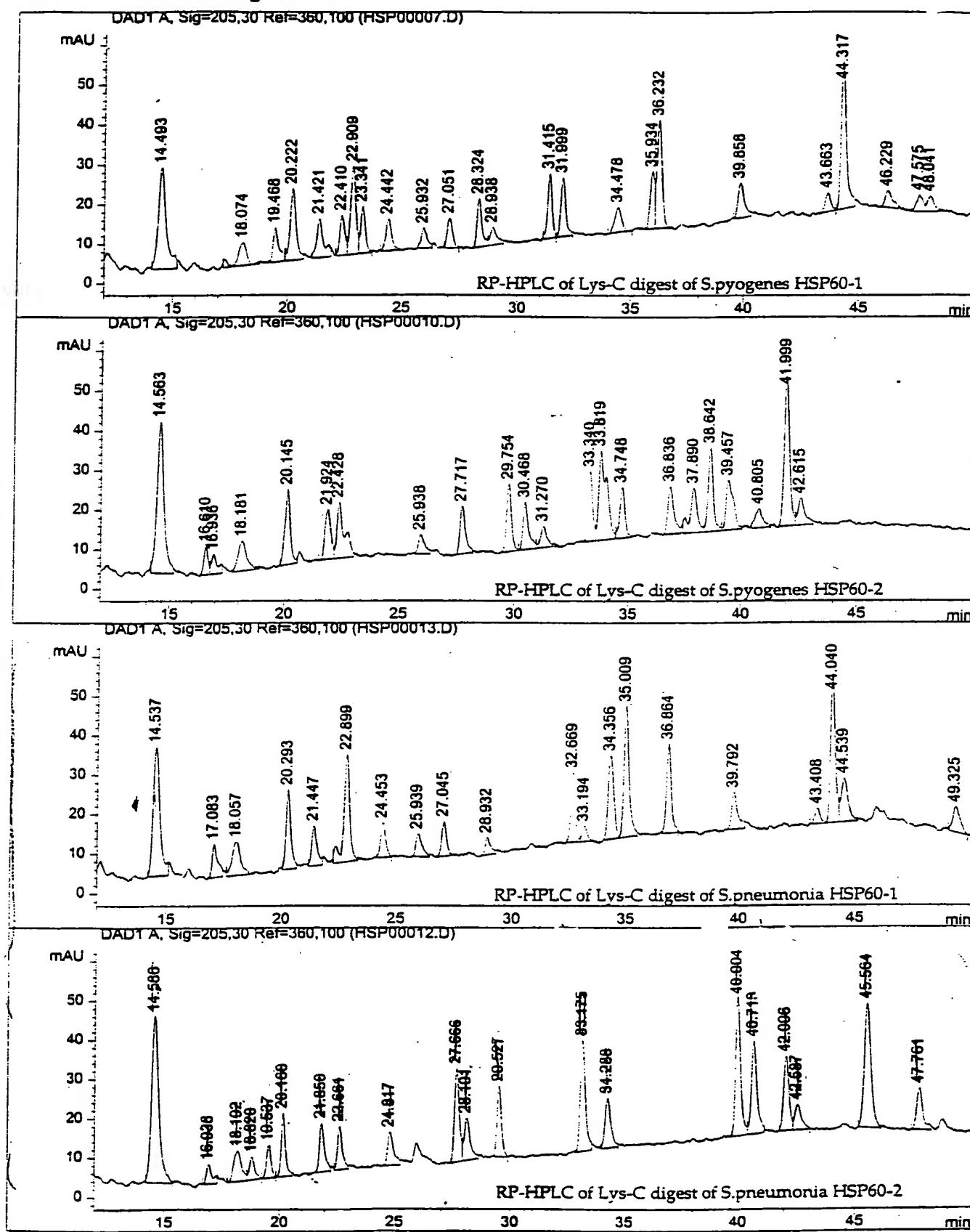


Figure 11